WHAT IS CLAIMED IS:

1. A method for identifying an individual having or at risk of devloping a neuropsychiatric disorder comprising the step of detecting the presence or absence of a mutation in the coding region of a human *HKNG1* gene having the nucleotide sequence depicted in SEQ ID NO:7, wherein a presence of a mutation in the coding region of the human *HKNG1* gene indicates that the individual has or is at risk of devloping a neuropsychiatric disorder.

2. The method of Claim 1, wherein the mutation results in production of a protein comprising an amino acid sequence which is different from the amino acid sequence depicted in SEQ ID NO:2.

3. The method of Claim 1, wherein the mutation results in production of a protein comprising an amino acid sequence that is different from the amino acid sequence of SEQ ID NO:4.

4. The method of Claim 1, wherein the mutation is detected in exon 7 of the *HKNG1* gene.

5. The method of Claim 2, wherein the mutation is detected in exon 7 of the *HKNG1* gene.

6. The method of Claim 3, wherein the mutation is detected in exon 7 of the *HKNG1* gene.

7. The method of Claim 2, wherein the mutation results in the substitution of a lysine for a glutamic acid at amino acid residue 202 of SEQ ID NO:2.

8. The method of Claim 3, wherein the mutation results in the substitution of a lysine for a glutamic acid at amino acid residue 184 of SEQ ID NO:4.

9. The method of Claim 1, wherein the method comprises the step of analyzing the sequence of the coding region of the human *HKNG1* gene by preparing and sequencing cDNA comprising a sequence that hybridizes under stringent conditions to the complement of a nucleotide sequence which encodes the polypeptide sequence depicted in SEQ ID NO:2.

10. The method of Claim 9, wherein the nucleotide sequence which encodes the polypeptide sequence depicted in SEQ ID NO:2 is the nucleotide sequence depicted in SEQ ID NO:1.

11. The method of Claim 1, wherein the method comprises the step of amplifying nucleic acid sequences using the polymerase chain reaction to detect the presence or absence of a mutation in the human *HKNG1* gene.

12. The method of Claim 1, wherein the method comprises a step of detecting the presence or absence of a mutation in the human *HKNG1* gene using SSCP.

13. The method of Claim 4, wherein the method uses primers selected from the group consisting of:

t t t a t t c c a t t t c t g t c c c c t a c (SEQ ID NO:22);
a a g g c t c a g t t a g g t c t g t a t c (SEQ ID NO:23);
c a g g a g t t t t a a c g t c t t c a g a c (SEQ ID NO:24); and
g a c t c a g a a a t g t c t a c c a t t t c (SEQ ID NO:25).

14. The method of Claim 5, wherein the method uses primers selected from the group consisting of:

t t t a t t c c a t t t c t g t c c c c t a c (SEQ ID NO:22);
a a g g c t c a g t t a g g t c t g t a t c (SEQ ID NO:23);

caggagttttaacgtcttcagac (SEQ ID NO:24); and

gactcagaaatgtctaccatttc (SEQ ID NO:25).

15. The method of Claim 6, wherein the method uses primers selected from the group consisting of:

tttattccatttctgtcccctac (SEQ ID NO:22);

aaggctcagttaggtctgtatc (SEQ ID NO:23);

caggagttttaacgtcttcagac (SEQ ID NO:24); and

gactcagaaatgtctaccatttc (SEQ ID NO:25).

16. The method of Claim 7, wherein the method uses primers selected from the group consisting of:

tttattccatttctgtcccctac (SEQ ID NO:22);

aaggctcagttaggtctgtatc (SEQ ID NO:23);

caggagttttaacgtcttcagac (SEQ ID NO:24); and

gactcagaaatgtctaccatttc (SEQ ID NO:25).

17. The method of Claim 8, wherein the method uses primers selected from the group consisting of:

tttattccatttctgtcccctac (SEQ ID NO:22);

aaggctcagttaggtctgtatc (SEQ ID NO:23);

caggagttttaacgtcttcagac (SEQ ID NO:24); and

gactcagaaatgtctaccatttc (SEQ ID NO:25).

18. The method of Claim 11, wherein the method uses primers selected from the group consisting of:

tttattccatttctgtcccctac (SEQ ID NO:22);

aaggctcagttaggtctgtatc (SEQ ID NO:23);

caggagttttaacgtcttcagac (SEQ ID NO:24); and

gactcagaaatgtctaccatttc (SEQ ID NO:25).

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